



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/632,694A

DATE: 10/04/2004

TIME: 11:02:44

Input Set : A:\New SURR113.ST25.txt

Output Set: N:\CRF4\10042004\J632694A.raw

3 <110> APPLICANT: Allison, Anthony  
 5 <120> TITLE OF INVENTION: MODIFIED ANNEXIN PROTEINS AND METHODS FOR TREATING VASO-  
 OCCLUSIVE

6 SICKLE-CELL DISEASE  
 8 <130> FILE REFERENCE: SURR.113  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/632,694A  
 C--> 10 <141> CURRENT FILING DATE: 2003-08-01  
 10 <150> PRIOR APPLICATION NUMBER: 60/400,718  
 11 <151> PRIOR FILING DATE: 2002-08-02  
 13 <150> PRIOR APPLICATION NUMBER: 10/080,370  
 14 <151> PRIOR FILING DATE: 2002-02-21  
 16 <160> NUMBER OF SEQ ID NOS: 9  
 18 <170> SOFTWARE: PatentIn version 3.2  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 957  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <400> SEQUENCE: 1

26 gcacagggttc tcagaggcac tgtgactgac ttccctggat ttgatgagcg ggctgatgca 60  
 28 gaaactcttc ggaaggctat gaaaggcttg ggcacagatg aggagagcat cctgactctg 120  
 30 ttgacatccc gaagtaatgc tcagcgccag gaaatctctg cagctttaa gactctgtt 180  
 32 ggcagggtat ttctggatga cctgaaatca gaactaactg gaaaatttga aaaattaatt 240  
 34 gtggctctga tggaaaccctc tcggctttat gatgctttag aactgaaaca tgccttgaag 300  
 36 ggagctggaa caaatgaaaa agtactgaca gaaattatttgc ttcaaggac acctgaagaa 360  
 38 ctgagagcca tcaaacaagt ttatgaagaa gaatatggct caagcctgga agatgacgtg 420  
 40 gtggggaca cttcagggtt ctaccagcg 480  
 42 gaccctgatg ctggaatgt tgaagctcaa 540  
 44 gctggagaac taaaatgggg gacagatgaa gaaaagtttgc tcaaccatctt tggAACACGA 600  
 46 agtgtgtctc atttgagaaaa ggtgtttgac aagtacatga ctatatcagg atttcaaatt 660  
 48 gaggaaacca ttgaccgcga gacttctggc aatttagagc aactactcct tgctgttg 720  
 50 aaatctattc gaagtataacc tgcctacattt gcagagaccc tctattatgc tatgaaggga 780  
 52 gctgggacag atgatcatc cctcatcaga gtcatggttt ccaggagtga gattgatctg 840  
 54 tttAACATCA ggaaggagtt taggaagaat tttgccacct ctctttattc catgatTAAG 900  
 56 ggagatacat ctggggacta taagaaagct ttctgctgc tctgtggaga agatgac 957  
 59 <210> SEQ ID NO: 2  
 60 <211> LENGTH: 957  
 61 <212> TYPE: DNA  
 62 <213> ORGANISM: Homo sapiens  
 65 <220> FEATURE:  
 66 <221> NAME/KEY: CDS  
 67 <222> LOCATION: (1)..(957)  
 69 <400> SEQUENCE: 2  
 70 gca cag gtt ctc aga ggc act gtg act gac ttc cct gga ttt gat gag 48  
 71 Ala Gln Val Leu Arg Gly Thr Val Thr Asp Phe Pro Gly Phe Asp Glu

6  
 ENTERED

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138 gtt tcc agg agt gag att gat ctg ttt aac atc agg aag gag ttt agg 864  
 139 Val Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg  
 140 275 280 285  
 142 aag aat ttt gcc acc tct ctt tat tcc atg att aag gga gat aca tct 912  
 143 Lys Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser  
 144 290 295 300  
 146 ggg gac tat aag aaa gct ctt ctg ctc tgt gga gaa gat gac 957  
 147 Gly Asp Tyr Lys Lys Ala Leu Leu Leu Cys Gly Glu Asp Asp  
 148 305 310 315

151 <210> SEQ ID NO: 3  
 152 <211> LENGTH: 319  
 153 <212> TYPE: PRT  
 154 <213> ORGANISM: Homo sapiens  
 156 <400> SEQUENCE: 3

158 Ala Gln Val Leu Arg Gly Thr Val Thr Asp Phe Pro Gly Phe Asp Glu  
 159 1 5 10 15  
 162 Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys Gly Leu Gly Thr  
 163 20 25 30  
 166 Asp Glu Glu Ser Ile Leu Thr Leu Leu Thr Ser Arg Ser Asn Ala Gln  
 167 35 40 45  
 170 Arg Gln Glu Ile Ser Ala Ala Phe Lys Thr Leu Phe Gly Arg Asp Leu  
 171 50 55 60  
 174 Leu Asp Asp Leu Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile  
 175 65 70 75 80  
 178 Val Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys  
 179 85 90 95  
 182 His Ala Leu Lys Gly Ala Gly Thr Asn Glu Lys Val Leu Thr Glu Ile  
 183 100 105 110  
 186 Ile Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Val Tyr  
 187 115 120 125  
 190 Glu Glu Glu Tyr Gly Ser Ser Leu Glu Asp Asp Val Val Gly Asp Thr  
 191 130 135 140  
 194 Ser Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg  
 195 145 150 155 160  
 198 Asp Pro Asp Ala Gly Ile Asp Glu Ala Gln Val Glu Gln Asp Ala Gln  
 199 165 170 175  
 202 Ala Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys  
 203 180 185 190  
 206 Phe Ile Thr Ile Phe Gly Thr Arg Ser Val Ser His Leu Arg Lys Val  
 207 195 200 205  
 210 Phe Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile  
 211 210 215 220  
 214 Asp Arg Glu Thr Ser Gly Asn Leu Glu Gln Leu Leu Ala Val Val  
 215 225 230 235 240  
 218 Lys Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr  
 219 245 250 255  
 222 Ala Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Met  
 223 260 265 270  
 226 Val Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg

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227	275	280	285
230	Lys Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser		
231	290	295	300
234	Gly Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Glu Asp Asp		
235	305	310	315

238 &lt;210&gt; SEQ ID NO: 4

239 &lt;211&gt; LENGTH: 2016

240 &lt;212&gt; TYPE: DNA

241 &lt;213&gt; ORGANISM: Artificial Sequence

243 &lt;220&gt; FEATURE:

244 &lt;223&gt; OTHER INFORMATION: primer

247 &lt;220&gt; FEATURE:

248 &lt;221&gt; NAME/KEY: misc\_feature

249 &lt;222&gt; LOCATION: (45)..(45)

250 &lt;223&gt; OTHER INFORMATION: n = a, c, t, or g

252 &lt;220&gt; FEATURE:

253 &lt;221&gt; NAME/KEY: misc\_feature

254 &lt;222&gt; LOCATION: (1000)..(1002)

255 &lt;223&gt; OTHER INFORMATION: n = a, c, t, or g

257 &lt;220&gt; FEATURE:

258 &lt;221&gt; NAME/KEY: misc\_feature

259 &lt;222&gt; LOCATION: (1051)..(1053)

260 &lt;223&gt; OTHER INFORMATION: n = a, c, t, or g

262 &lt;400&gt; SEQUENCE: 4

7--> 263	atggactaca aagacgtga cgacaagtt gggccgcga attcngccct ggcggcacc	60
265	gtgaccgact ttcggctt cgacggccgc ggcgacgccc aggtgtcgca caaggccatg	120
267	aagggcctgg gcaccgacga ggactccatc ctgaacctgc tgaccgcctg ctccaaacgc	180
269	cagcgcacgc agatcgccga ggagttcaag accctgttcg gcccgcaccc ggtgaacgac	240
271	atgaagtccg agctgaccgg caagttcgag aagctgatcg tggccctgtat gaagccctcc	300
273	cgcctgtacg acgcctacga gctgaagcac gccaagctgg ggcggccac cgacgagaag	360
275	gtgctgaccg agatcatcgc ctccgcacc cccgaggagc tgccgcacat caagcaggcc	420
277	tacgaggagg agtacggctc caacctggag gacgacgttg tggccgacac ctccggctac	480
279	taccagcga tgcgtgggt gctgctgcag gccaaccgcg accccgacac cgccatcgac	540
281	gacgcccagg tggagctgga cggccaggcc ctgttccagg cccggcagct gaagtggggc	600
283	accgacgagg agaagttcat caccatctg ggcacccgc cctgttccca cctgcgcgc	660
285	gtgttcgaca agtacatgac catctccggc ttccagatcg aggagaccat cgaccgcag	720
287	acctccggca acctggagaa cctgctgtg gccgtggta agtccatccg ctccatcccc	780
289	gcctacctgg ccgagaccct gtactacgc atgaaggcgcc cccggcaccga cgaccacacc	840
291	ctgatccgcg tgcgtgtc cccgtccgag atcgacctgt tcaacatccg caaggagttc	900
293	cgcaagaact tcgcccaccc cctgtactcc atgatcaagg gcgacaccc cggcgactac	960
7--> 295	aagaaggccc tgcgtgtgt gtcggcgcc gaggacgacn nnagatctcg atcggccctg	1020
7--> 297	gaggtgtgt tccaggggccc cggaaagtact nnngccctgc gccggcaccgt gaccgacttc	1080
299	tccggccctcg acggccgcgc cgacgcgcgag gtgcgtgcga aggccatgaa gggcctgggc	1140
301	accgacgagg actccatctt gaacctgtg accgcggccct ccaacgcaca ggcggcagcag	1200
303	atcgccgagg agttcaagac cctgttccgc cccgacccgt tgaacgacat gaagtccgag	1260
305	ctgaccggca agttcgagaa gctgatcgatg gccctgtatga agccctcccg cctgtacgac	1320
307	gcctacgagc tgaagcaccgc caagctggc gccggcaccg acgagaaggt gctgaccgag	1380
309	atcatcgccct cccgcaccccg cgaggagctg cccgacccatca agcaggccata cgaggaggag	1440
311	tacggctcca acctggagga cgacgtggta ggcgacaccc ccggctacta ccagcgcatt	1500

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313 ctgggtggtgc tgctgcaggc caaccgcgac cccgacaccg ccatcgacga cgcccaggtg 1560  
 315 gagctggacg cccaggccct gttccaggcc ggcgagctga agtggggcac cgacgaggag 1620  
 317 aagttcatca ccatcctggg caccgcgtcc gtgtcccacc tgccgcgcgt gttcqacaag 1680  
 319 tacatgacca tctccggctt ccagatcgag gagaccatcg accgcgagac ctccggcaac 1740  
 321 ctggagaacc tgctgctggc cgtggtaag tccatccgcgt ccatccccgc ctacctggcc 1800  
 323 gagaccctgt actacgcccattt gaagggcgcc ggcaccgcgt accacaccct gatccgcgtg 1860  
 325 atcgtgtccc gctccgagat cgacctgttc aacatccgcgtt aggagttccg caagaacttc 1920  
 327 gccacctccc tgtactccat gatcaaggcc gacacctccg gcgactacaa gaaggccctg 1980  
 329 ctgctgctgt gcggcgccgaa ggacgactaa taataa 2016  
 332 <210> SEQ ID NO: 5  
 333 <211> LENGTH: 2016  
 334 <212> TYPE: DNA  
 335 <213> ORGANISM: Artificial Sequence  
 337 <220> FEATURE:  
 338 <223> OTHER INFORMATION: primer  
 341 <220> FEATURE:  
 342 <221> NAME/KEY: CDS  
 343 <222> LOCATION: (1)..(2016)  
 345 <220> FEATURE:  
 346 <221> NAME/KEY: misc\_feature  
 347 <222> LOCATION: (45)..(45) /  
 348 <223> OTHER INFORMATION: n = a, c, t, or g  
 350 <220> FEATURE:  
 351 <221> NAME/KEY: misc\_feature  
 352 <222> LOCATION: (1000)..(1002) /  
 353 <223> OTHER INFORMATION: n = a, c, t, or g  
 355 <220> FEATURE:  
 356 <221> NAME/KEY: misc\_feature /  
 357 <222> LOCATION: (1051)..(1053) /  
 358 <223> OTHER INFORMATION: n = a, c, t, or g  
 360 <400> SEQUENCE: 5  
 -> 361 atg gac tac aaa gac gat gac aag ctt gcg gcc gcg aat tcn gcc 48  
 -> 362 Met Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Ala Ala Asn Xaa Ala  
 363 1 5 10 15  
 365 ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac 96  
 366 Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp  
 367 20 25 30  
 369 gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac 144  
 370 Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp  
 371 35 40 45  
 373 tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc cag cag 192  
 374 Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln  
 375 50 55 60  
 377 atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg aac gac 240  
 378 Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp  
 379 65 70 75 80  
 381 atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg gcc ctg 288  
 382 Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu  
 383 85 90 95

RAW SEQUENCE LISTING ERROR SUMMARY  
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caution Note:

One or more n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

q#:4; N Pos. 45,1000,1001,1002,1051,1052,1053

q#:5; N Pos. 45,1000,1001,1002,1051,1052,1053

q#:5; Xaa Pos. 15,334,351

q#:6; Xaa Pos. 15,334,351

valid <213> Response:

One or more "Artificial" only as "<213> Organism" response is incomplete, under 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

q#:9

**VERIFICATION SUMMARY**

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:960  
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1020  
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:48  
L:441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:960  
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1008  
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1008  
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1056  
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:320  
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:336